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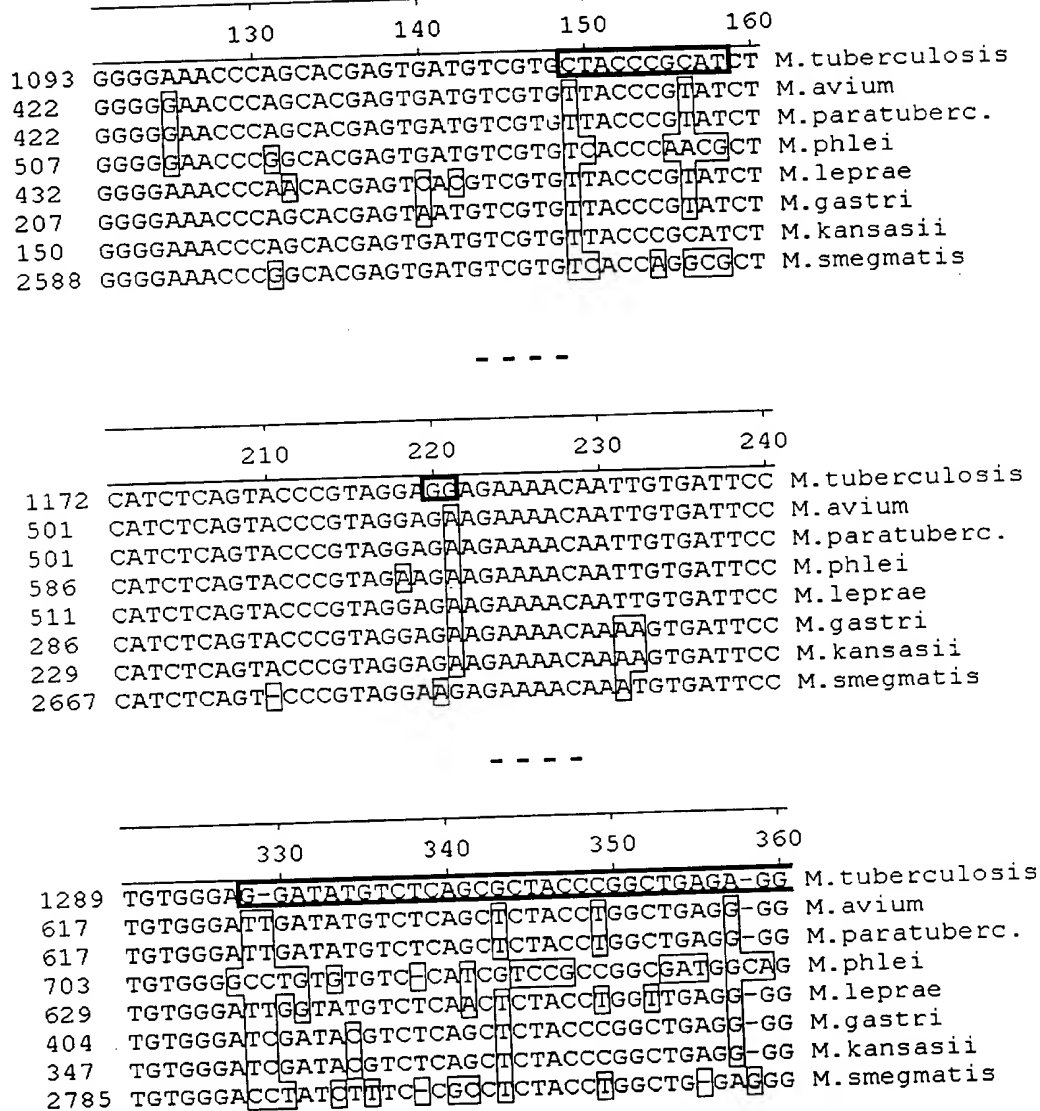


Figure 1A

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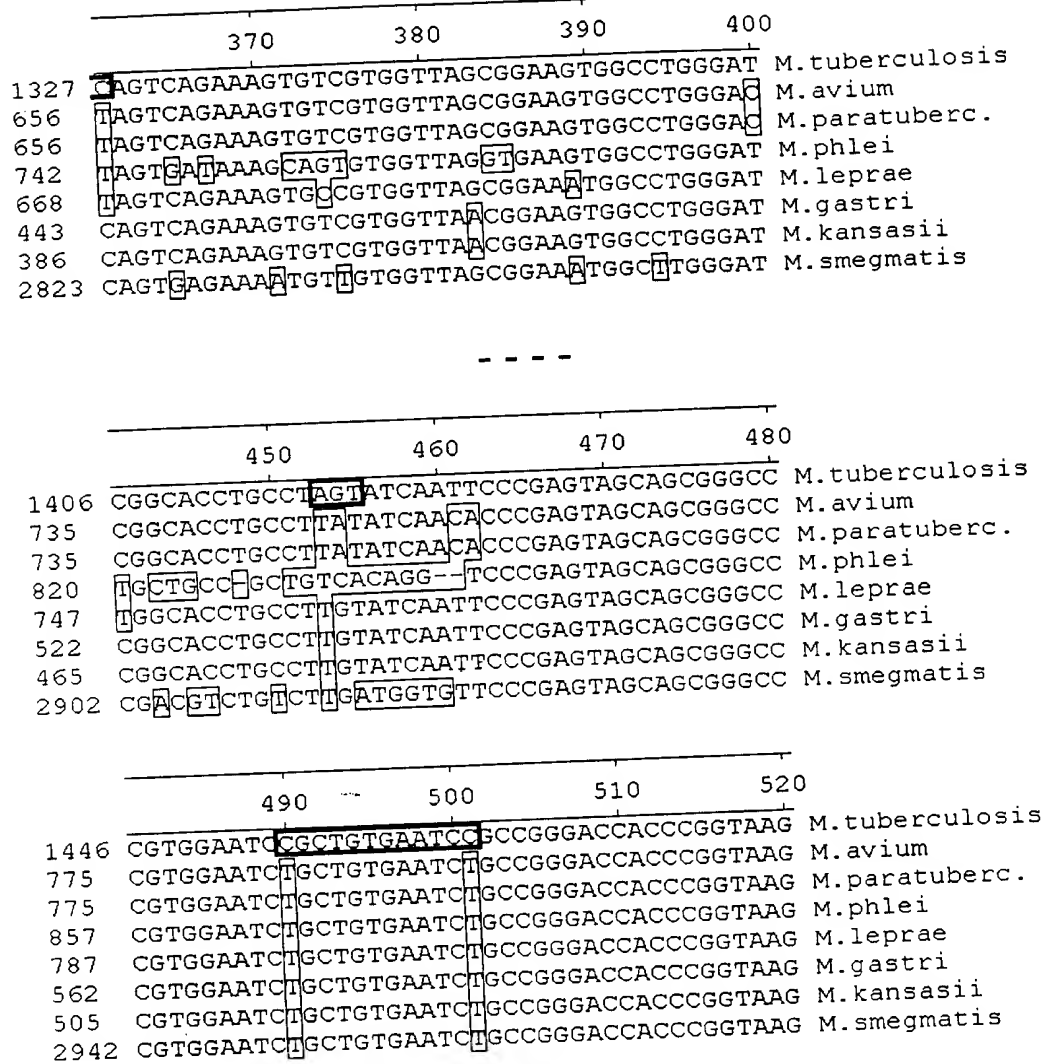


Figure 1B

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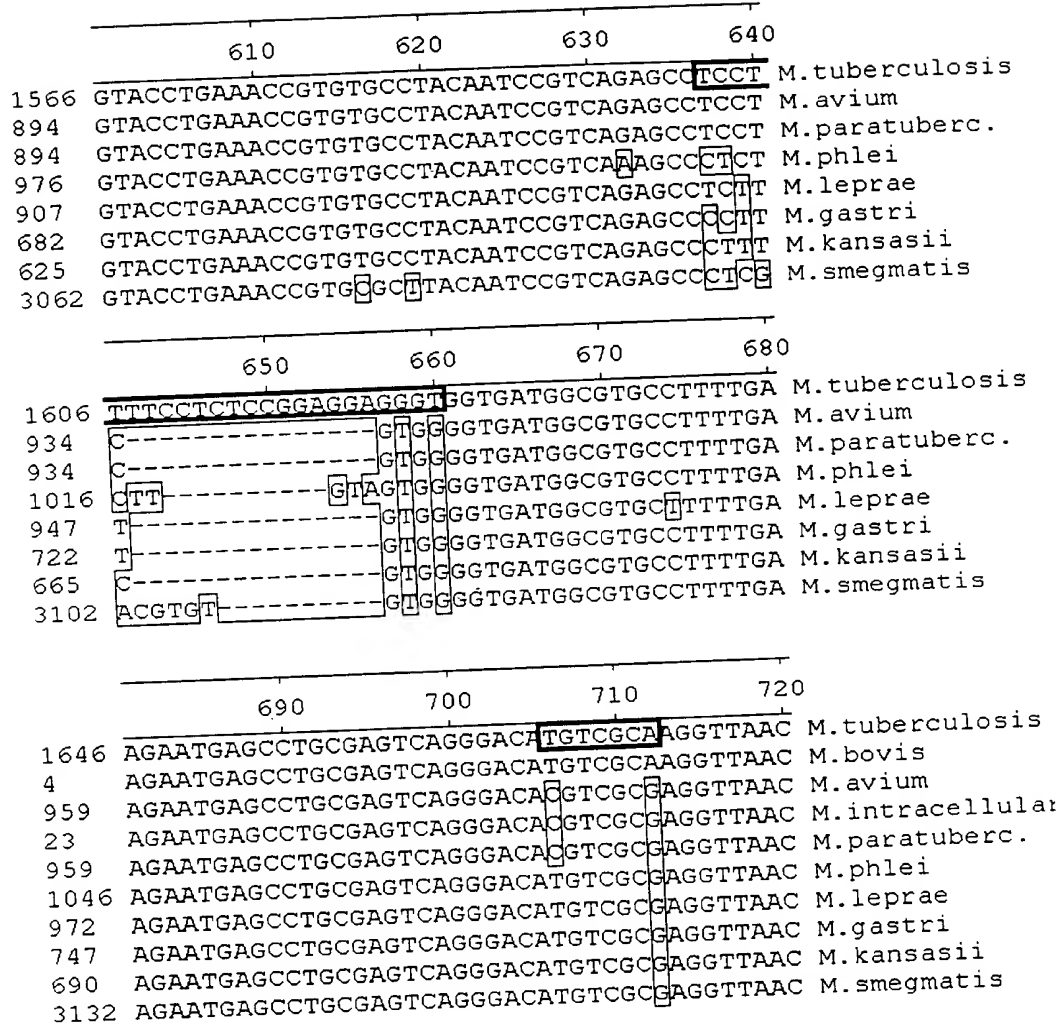


Figure 1C

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		770	780	790	800	
1726	CGACCCACACGCGCATACGCGCGTGTGAA					M.tuberculosis
84	CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT					M.bovis
1039	CG-----CATCCCTTTTGGGGTGT					M.avium
103	CG-----CATCCCTTTTGGGGTGT					M.intracellula
1039	CG-----CATCCCTTTTGGGGTGT					M.paratuberc.
1126	CGTATCCACCTGTTGGGGTTGGTGT					M.phlei
1052	CGTAT--CACGTTGTGAGCGTGTGT					M.leprae
827	CGTAT--CACGCGTAAGCGTGTGT					M.gastri
770	CGTAT--CGCGCGGAGCGTGTGT					M.kansasii
3212	CGTAT--CCACACAAGAGTGTGTGTGT					M.smegmatis

		970	980	990	1000	
1926	ATTTAGGTGCAGCGTTGCGTGGTTCACCG					M.tuberculosis
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCG					M.avium
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCG					M.paratuberc.
1322	ATTTAGGTGCAGCGTGGCTGTTTCTTATCGGAGGTAGAG					M.phlei
1244	ATTTAGGTGCAGCGTTGCGTGGTTCACCG					M.leprae
1019	ATTTAGGTGCAGCGTTGCGTGGTTCACCG					M.gastri
962	ATTTAGGTGCAGCGTTGCGTGGTTCACCG					M.kansasii
3408	ATTTAGGTGCAGCGTGGCTGTTTCTTGC					M.smegmatis

		1050	1060	1070	1080	
2005	CAGCCAAACTCCGAATGCCG-TGGTG-TA-AA					M.tuberculosis
1307	CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA					M.avium
1307	CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA					M.paratuberc.
1401	CAGCCAAACTCCGAATGCCG-TAAG-TAAAAGTGGCA					M.phlei
1323	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA					M.leprae
1098	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA					M.gastri
1041	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA					M.kansasii
3486	CAGCCAAACTCCGAATGCCG-TAAGGCAAGAGTGGCA					M.smegmatis

Figure 1D

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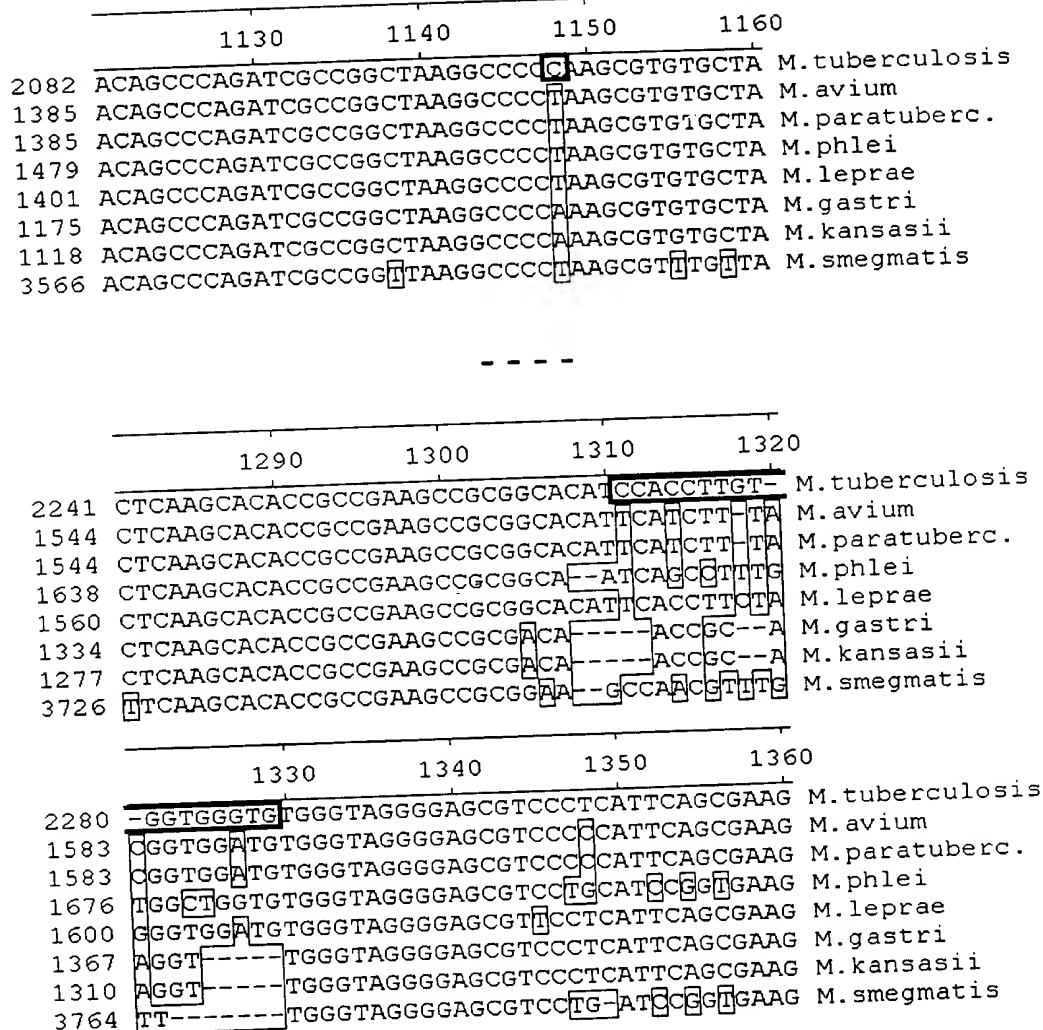


Figure 1E

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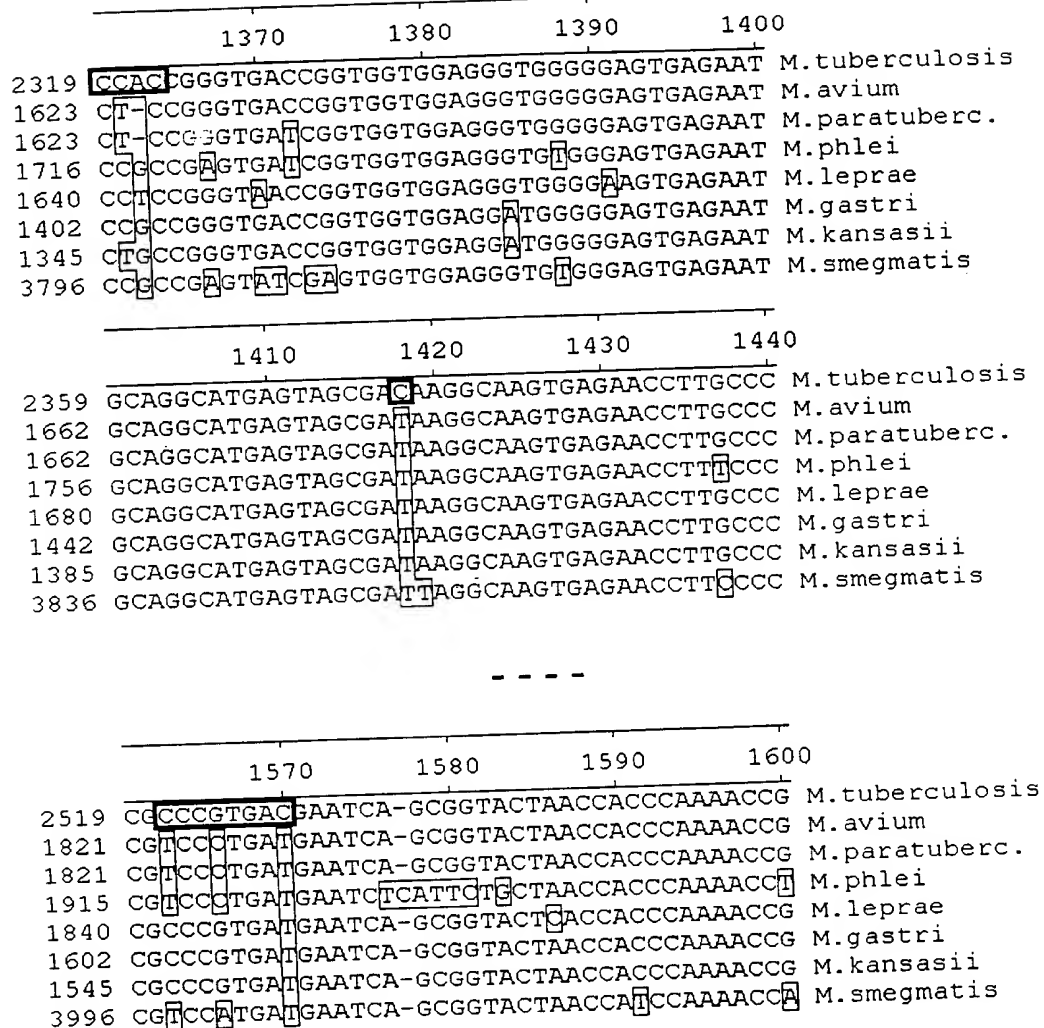


Figure 1F

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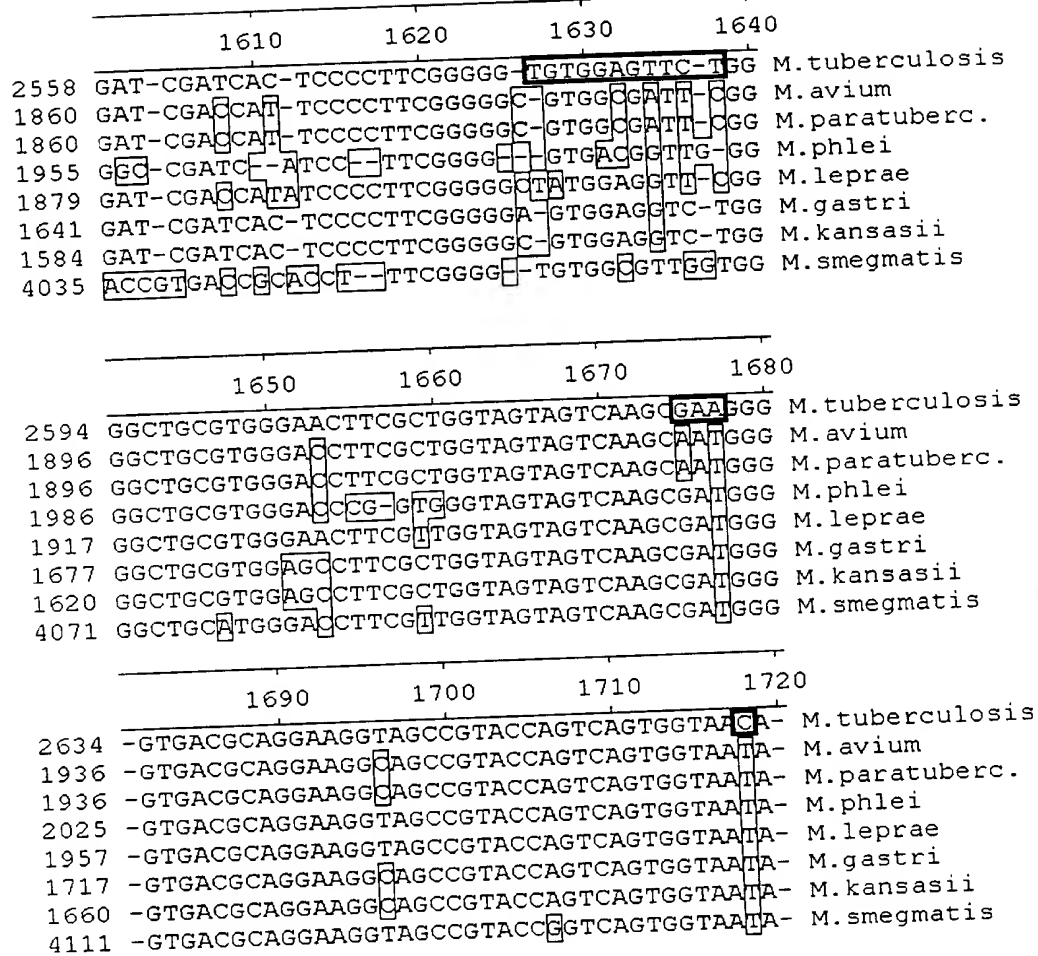


Figure 1G

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1730 1740 1750 1760

2672 -CTGGGGCAAGCCGGTAGGGAGAGCGATAGGCAAATCCGT M.tuberculosis
 1974 -CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT M.avium
 1974 -CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT M.paratuberc.
 2063 -CGGGGGTAAACCTGTAGGGGAGAGGATAGGCAAATCCGT M.phlei
 1995 -CTGGAGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.leprae
 1755 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.gastri
 1698 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.kansasii
 4149 -CGGGGTAAAGCCGTGTAGGGAGTCAGATAGGTTAAATCCGT M.smegmatis

1970 1980 1990 2000

2908 AGGGGGACCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.tuberculosis
 2208 AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.avium
 2208 AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.paratuberc.
 2298 AGGGGGACCCACGTACCGTGAGGGCTCTTGCGGGGGAGC M.phlei
 2231 AGGGGGCCCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.leprae
 1910 M.gastri
 1934 AGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.kansasii
 4385 AGGGGGACCCACATGGCGTGTAAAGCCTTTACGGCCCAAGC M.smegmatis

2410 2420 2430 2440

3345 ACCTCGACGCCAGTTGGGGCGGAGTCGTTGTTGAAATACC M.tuberculosis
 284 ACCTCGACGCCAGTTGGGGCGGAGTCGTTGTTGAAATACC M.bovis
 2645 GCACAGACGCCAGTTGGTGGAGTCGTTGTTGAAATACC M.avium
 393 ATACAGACGCCAGTTGTATGGAGTCGTTGTTGAAATACC M.intracellulare
 2645 GCACAGACGCCAGTTGGTGGAGTCGTTGTTGAAATACC M.paratuberc.
 2737 GCTCGGACGCCAGTTGGGTGGAGTCGTTGTTGAAATACC M.phlei
 2668 ACCTCGACGCCAGTTGGGTGGAGTCGTTGTTGAAATACC M.leprae
 1910 M.gastri
 2372 ACCTCAACGCCAGTTGGGGTGGAGTCGTTGTTGAAATACC M.kansasii
 4822 GCTCACAGGCCAGTTGGGTGGAGTCGTTGTTGAAATACC M.smegmatis

Figure 1H

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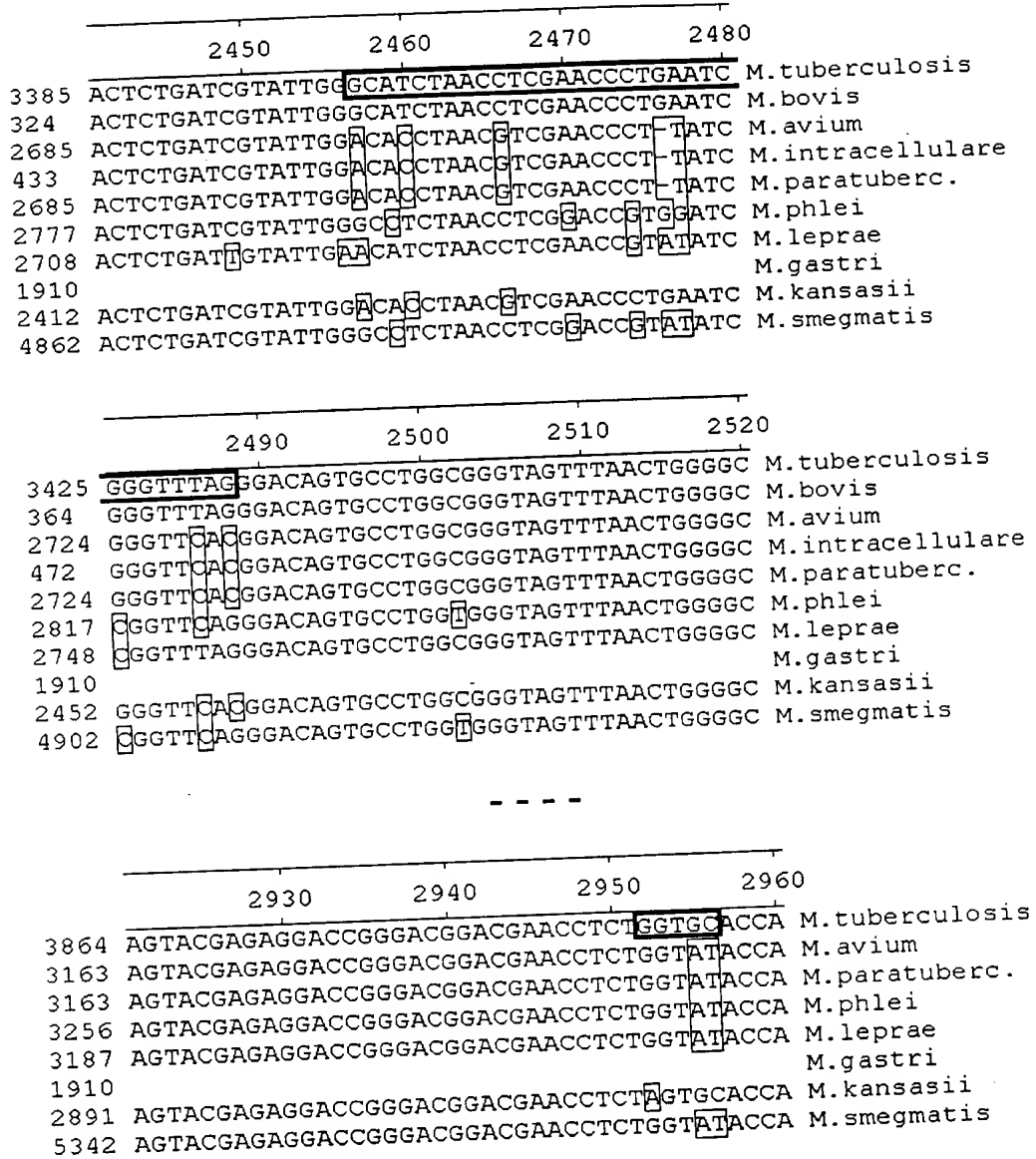


Figure 11

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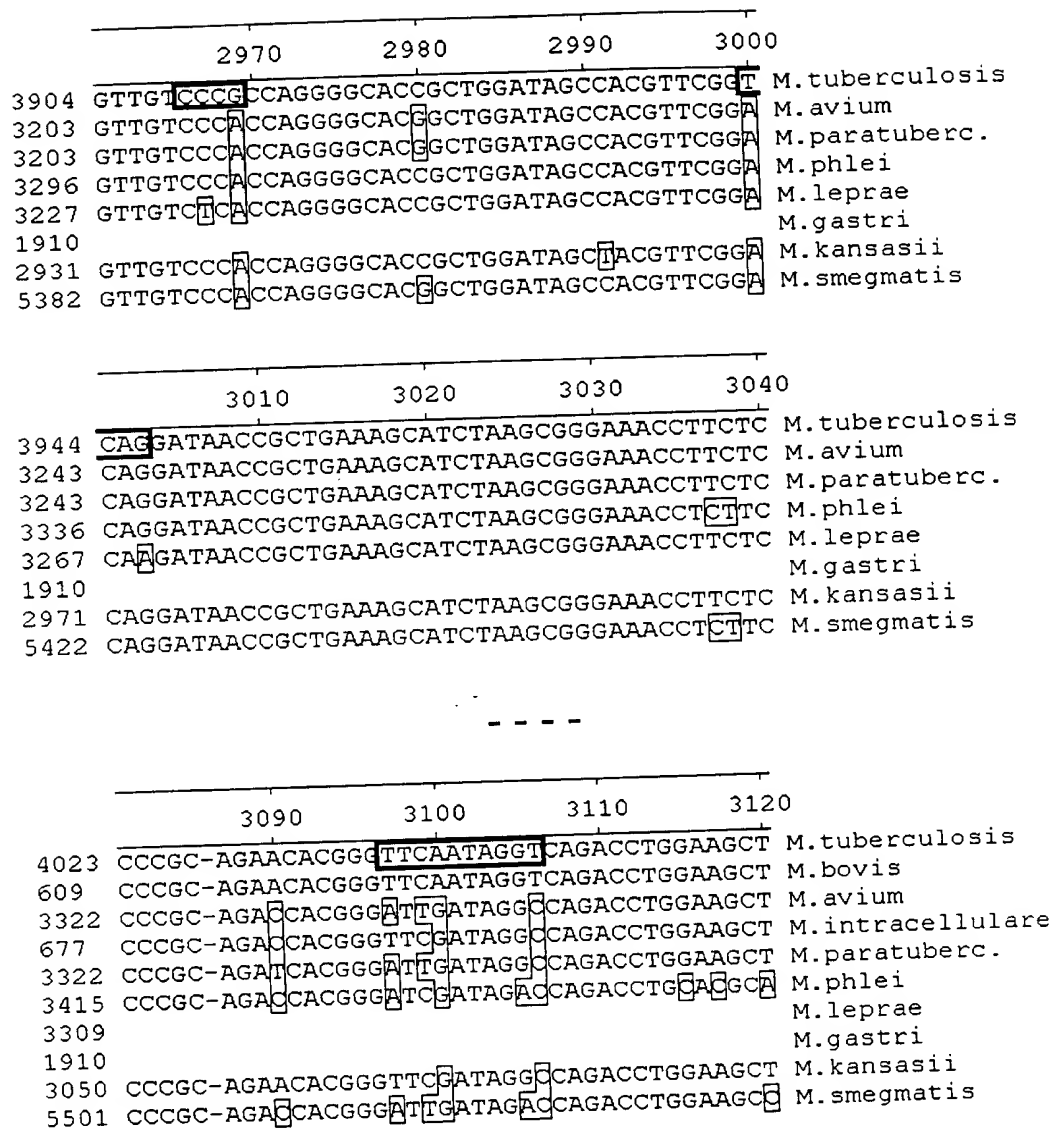


Figure 1J

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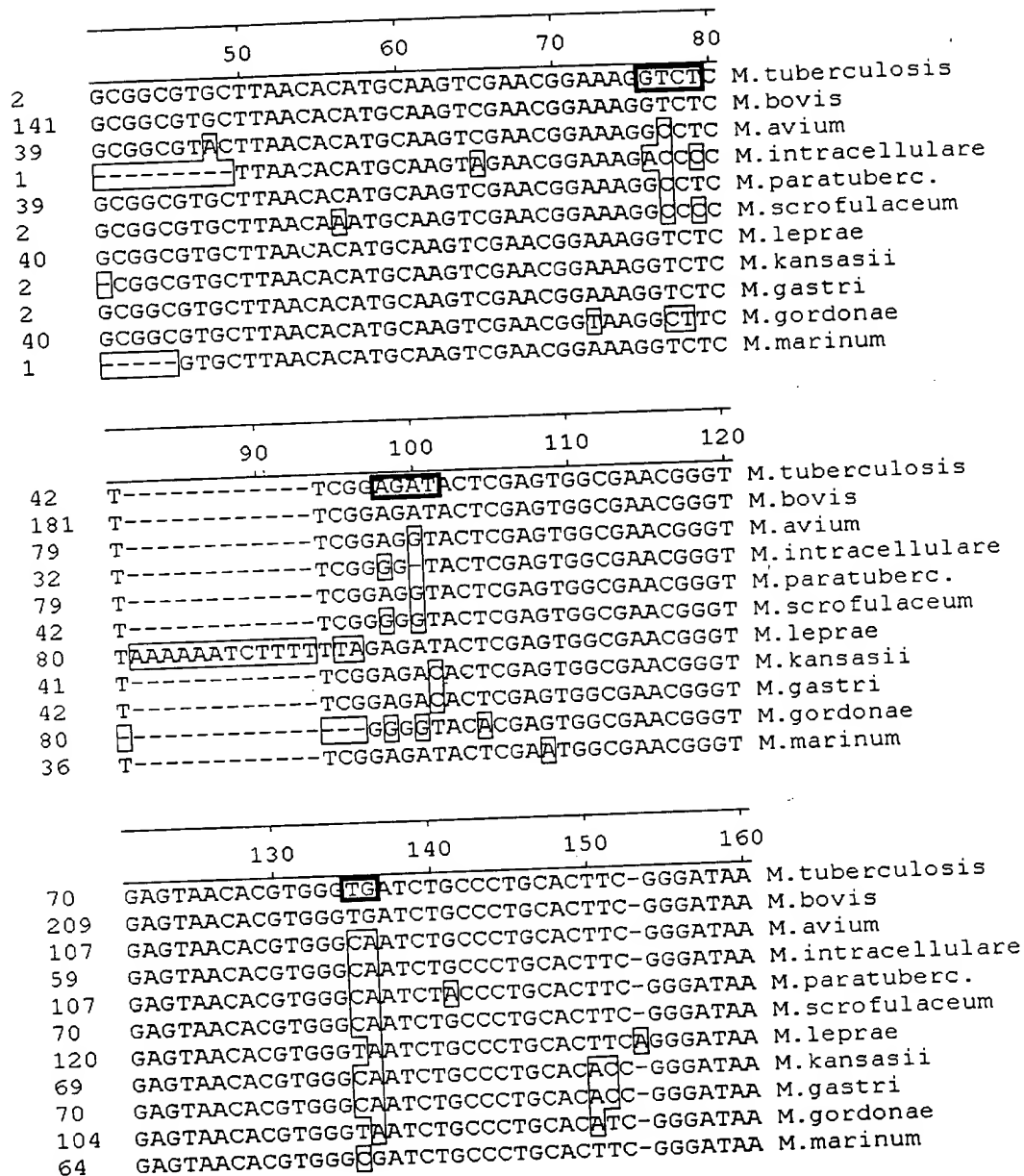


Figure 2A

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	170	180	190	200	
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGAC	CACGGGA			M.tuberculosis
248	GCCTGGGAAACTGGGTCTAATACCGGATAGGACC	CACGGGA			M.bovis
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCT	CAAGA			M.avium
98	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCT	TTAGG			M.intracellulare
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCT	CAAGA			M.paratuberc.
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACC	ACTTGG			M.scrofulaceum
160	GCCTGGGAAACTGGGTCTAATACCGGATAGGAC	TTCAAGG			M.leprae
108	GCCTGGGAAACTGGGTCTAATACCGGATAGGACC	ACTTGG			M.kansasii
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACC	ACTTGG			M.gastri
143	GCCTGGGAAACTGGGTCTAATACCGGATAGGACC	ACGGGA			M.gordonae
103	GCCTGGGAAACTGGGTCTAATACCGGATAGGACC	ACGGGA			M.marinum

	210	220	230	240	
149	TGCATGTCTTGTGGTGGAAAG	CGCTTTAG	CGGTGTGGGAT		M.tuberculosis
288	TGCATGTCTTGTGGTGGAAAGCGCTTTAG	CGGTGTGGGAT			M.bovis
186	CGCATGTCTTTGGTGGAAAGC	TTTT	ACGGTGTGGGAT		M.avium
138	CGCATGTCTTTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.intracellulare
186	CGCATGTCTTTGGTGGAAAGC	TTTT	GCGGTGTGGAT		M.paratuberc.
149	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.scrofulaceum
200	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGCGAGGAT		M.leprae
148	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.kansasii
149	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.gastri
183	CACATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.gordonae
143	TTCATGTCTTGTGGTGGAAAG	CTTT	GCGGTGTGGGAT		M.marinum

	250	260	270	280	
189	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	ACGGCCT			M.tuberculosis
328	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	ACGGCCT			M.bovis
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	ACGGCCT			M.avium
176	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	AGGCCT			M.intracellulare
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	ACGGCCT			M.paratuberc.
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	AGGCCT			M.scrofulaceum
239	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	ACGGCCT			M.leprae
186	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	ACGGCCT			M.kansasii
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	AGGCCT			M.gastri
221	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	AGGCCT			M.gordonae
181	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTG	ACGGCCT			M.marinum

Figure 2B

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450 460 470 480

389 AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG M.tuberculosis
 528 AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG M.bovis
 424 AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG M.avium
 376 AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG M.intracellulare
 424 AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTAGG M.paratuberc.
 387 AAACCTCTTTTACCATCGACGAAGGTCTCA---CTTTGTGG M.scrofulaceum
 439 AAACCTCTTTTACCATCGACGAAGGTCTGGGAATTCTCTCGG M.leprae
 386 AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG M.kansasii
 387 AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG M.gastri
 420 AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG M.gordonae
 381 AAACCTCTTTTACCATCGACGAAGGTCTGGGTTCTCTCGG M.marinum

1130 1140 1150 1160

1069 TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG M.tuberculosis
 1208 TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG M.bovis
 1104 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.avium
 1056 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.intracellulare
 1098 TCTCATGTTGCCAGCGGGTAATGCCAGGGGACTCGTGAGAG M.paratuberc.
 1064 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.scrofulaceum
 1119 TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG M.leprae
 1066 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.kansasii
 1067 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.gastri
 1100 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.gordonae
 1061 TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG M.marinum

1250 1260 1270 1280

1189 CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG M.tuberculosis
 1328 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG M.bovis
 1224 CAATGGCCGGTACAAAGGGCTGCGATGCCGTAAGGTTAAG M.avium
 1176 CAATGGCCGGTACAAAGGGCTGCGATGCCGTAAGGTTAAG M.intracellulare
 1218 CAATGGCCGGTACAAAGGGCTGCGATGCCGTAAGGTTAAG M.paratuberc.
 1184 CAATGGCCGGTACAAAGGGCTGCGATGCCGTAAGGTTAAG M.scrofulaceum
 1239 CAATGGCCGGTACAAAGGGCTGCGATGCCGTAAGGTTAAG M.leprae
 1186 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG M.kansasii
 1187 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG M.gastri
 1220 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG M.gordonae
 1181 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG M.marinum

Figure 2C

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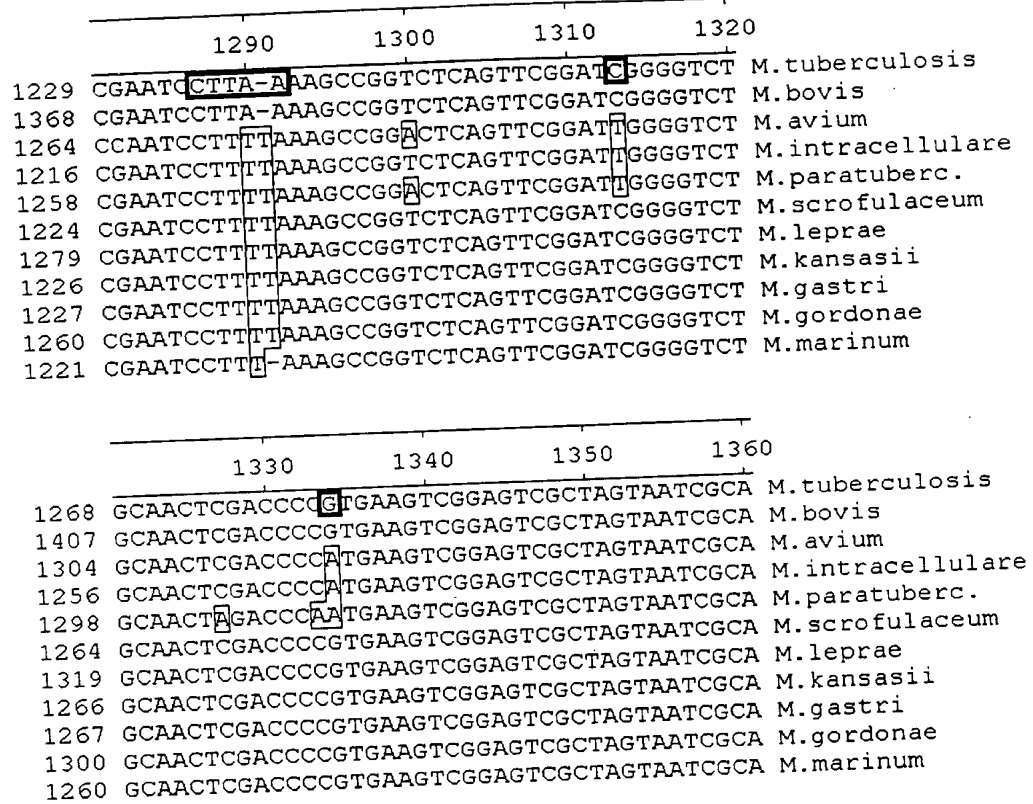


Figure 2D

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	50	60	70	80	
128	TTCCGA	ACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC			M.tuberculosis
39	TG	CCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC			M.bovis
41	T	CCGAACCCGGAAGCTAAGCCTGCCAGCGCCATGATAC			M.phlei
3559	T	ACCGAACCCGGAAGCTAAGCCTGTCAGCGCCGATGATAC			M.leprae
5743	T	CCGAACCCGGAAGCTAAGCCTGCCAGC	CCGATGATAC		M.smegmatis

	90	100	110	120			
168	TGCCC	CTCCG	SG	---	TGGAAAAGTAGGACACCGCCGAAC	M.tuberculosis	
79	TGCCCC	TCCGGG	---		TGGAAAAGTAGGACACCGCCGAAC	M.bovis	
81	TGCCCC	TCAC	GGG	---	TGGAAAAGTAGGACACCGCCGAAC	M.phlei	
3599	TGCCCC	ATTCGGG	---		TGGAAAAGTAGGACACCGCCGAAC	M.leprae	
5782	T	ACCC	TT	CCGGG	---	TGGAAAAGTAGGACACCGCCGAAC	M.smegmatis

Figure 3

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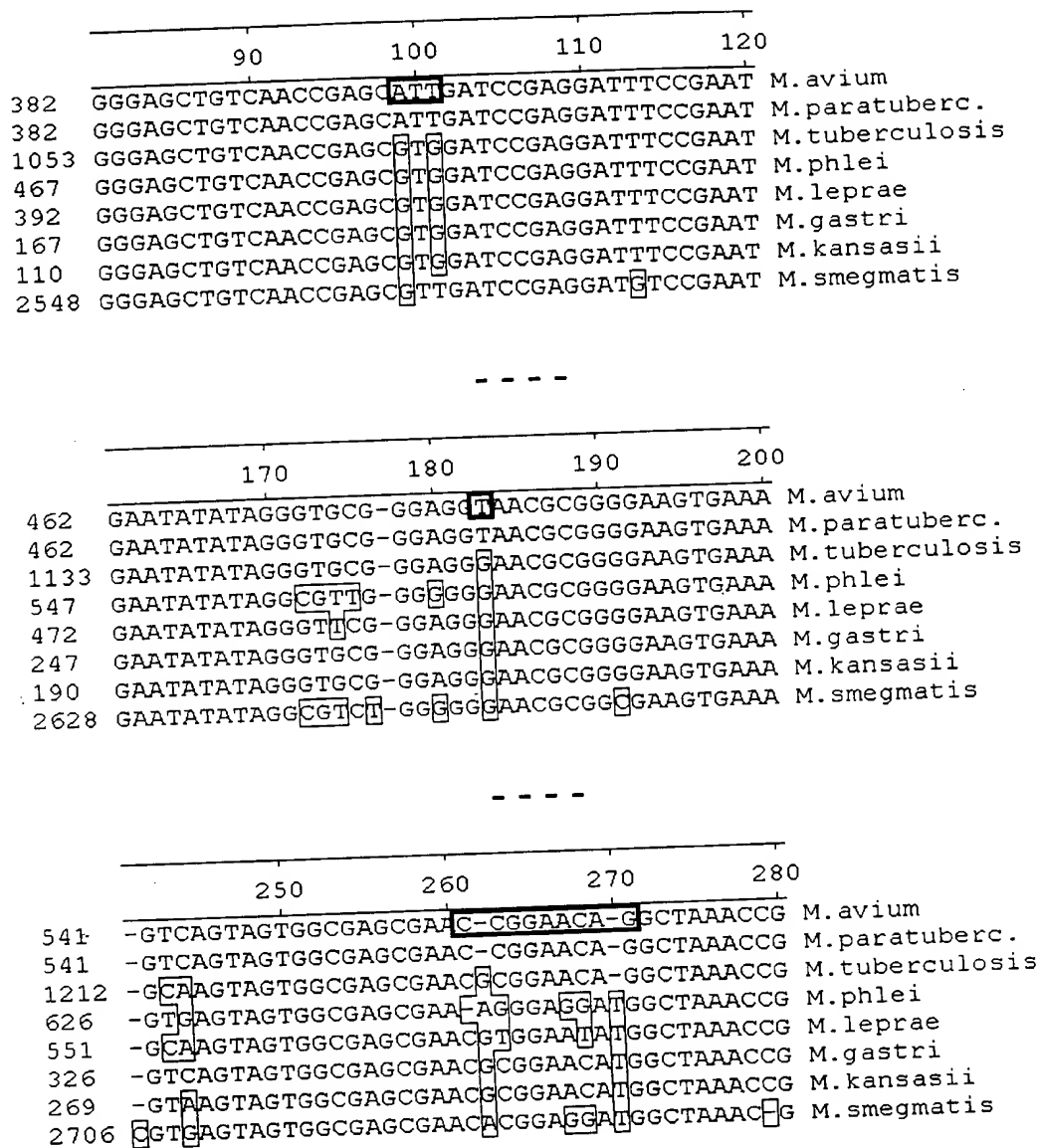


Figure 4A

17/31

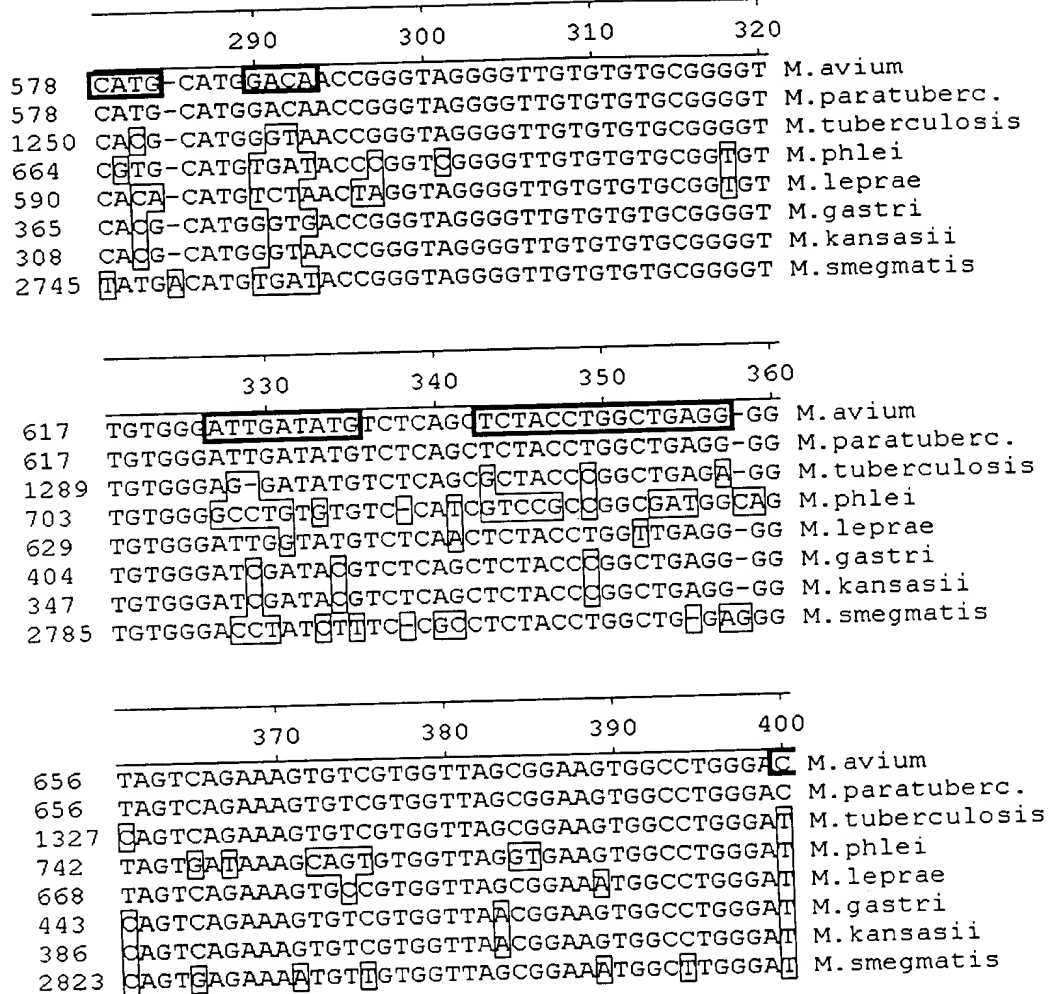


Figure 4B

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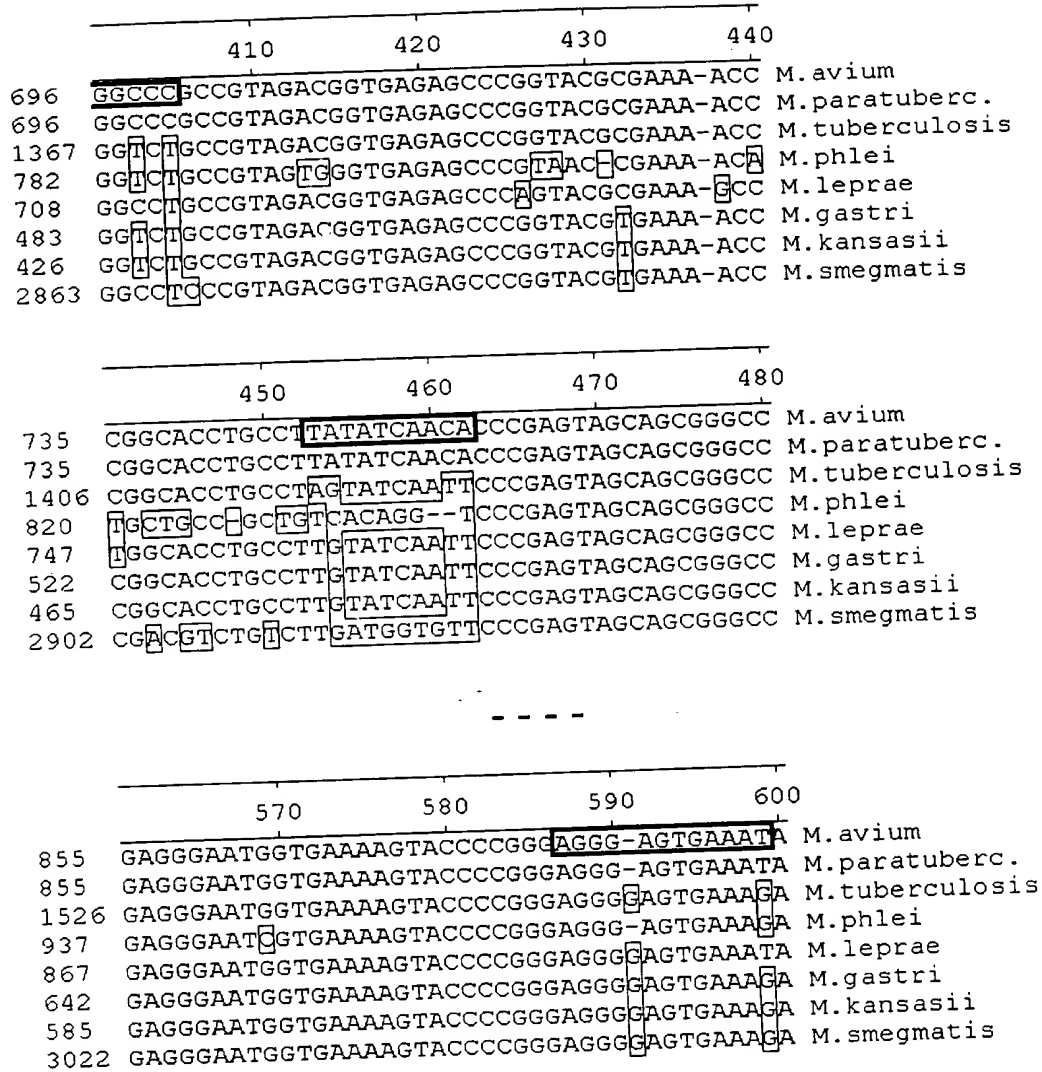


Figure 4C

19/31

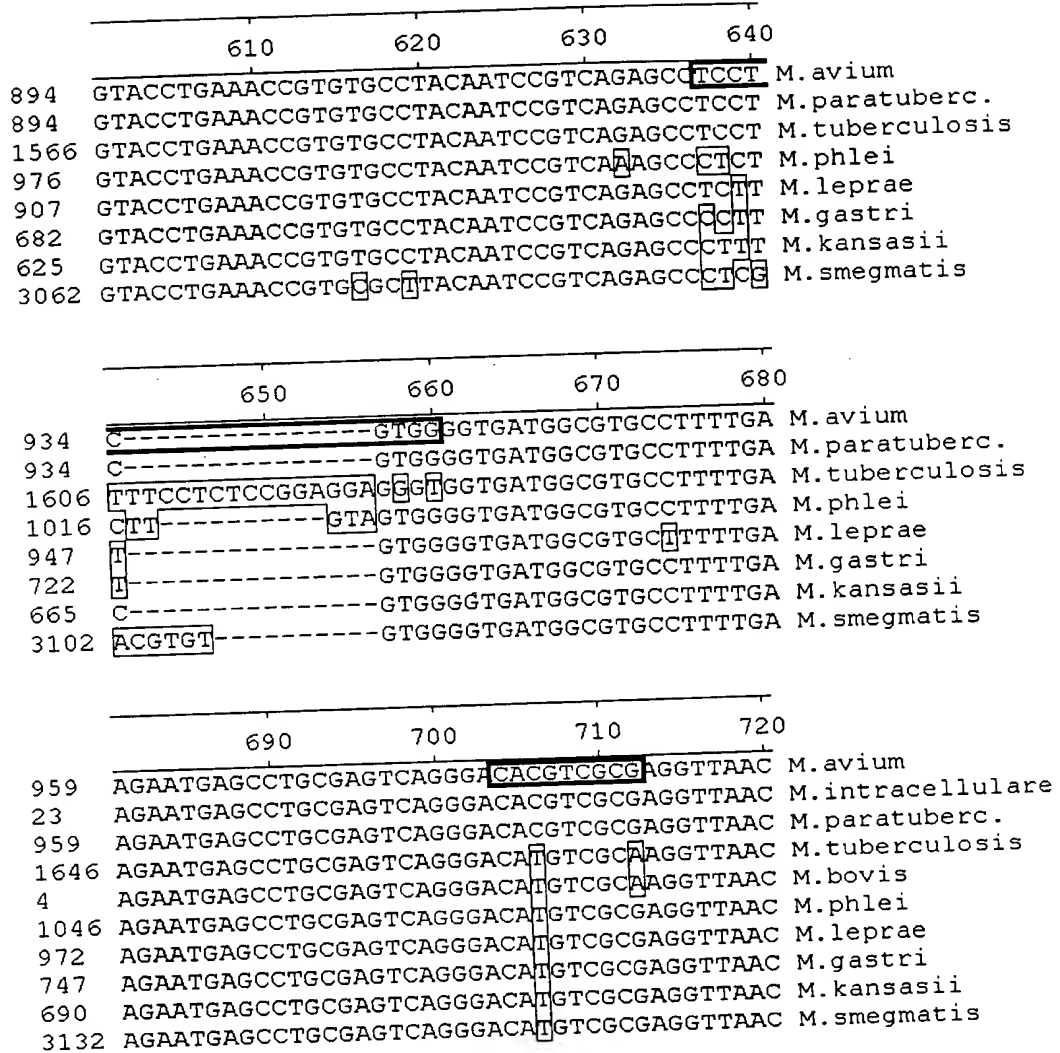


Figure 4D

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770 780 790 800

1039 CGCATCCCCTTTGGG-----GTGTAGTGGCGTGT M.avium
 103 CGCATCCCCTTTGGG-----GTGTAGTGGCGTGT M.intracellulare
 1039 CGCATCCCCTTTGGG-----GTGTAGTGGCGTGT M.paratuberc.
 1726 CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT M.tuberculosis
 84 CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT M.bovis
 1126 CGTATCCCAACCTGTT-----EGGGTTGTTGTAGTGGCGTGT M.phlei
 1052 CGTATCACGTTGTGAGCGT-----GTGTAGTGGCGTGT M.leprae
 827 CGTATCACGCGTAAGCGT-----GTGTAGTGGCGTGT M.gastri
 770 CGTATCGCGCGCGAGCGT-----GTGTAGTGGCGTGT M.kansasii
 3212 CGTATCCACACAAGAGTGTGTG-----GTGTAGTGGCGTGT M.smegmatis

1050 1060 1070 1080

1307 CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA M.avium
 1307 CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA M.paratuberc.
 2005 CAGCCAAACTCCGAATGCCG-TGGTG-TAAGCGTGGCA M.tuberculosis
 1401 CAGCCAAACTCCGAATGCCG-TAAG-TAAAAGTGTGGCA M.phlei
 1323 CAGCCAAACTCCGAATGCCG-TGGTT-TAAAAGCGTGGCA M.leprae
 1098 CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA M.gastri
 1041 CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA M.kansasii
 3486 CAGCCAAACTCCGAATGCCG-TAAGGCCAAGAGTGGGAA M.smegmatis

1170 1180 1190 1200

1425 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.avium
 1425 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.paratuberc.
 2122 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.tuberculosis
 1519 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.phlei
 1441 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.leprae
 1215 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.gastri
 1158 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.kansasii
 3606 AGTGGAAAAGGATGTGTAGTCGCAGAGAGAAACCAGGAGG M.smegmatis

Figure 4E

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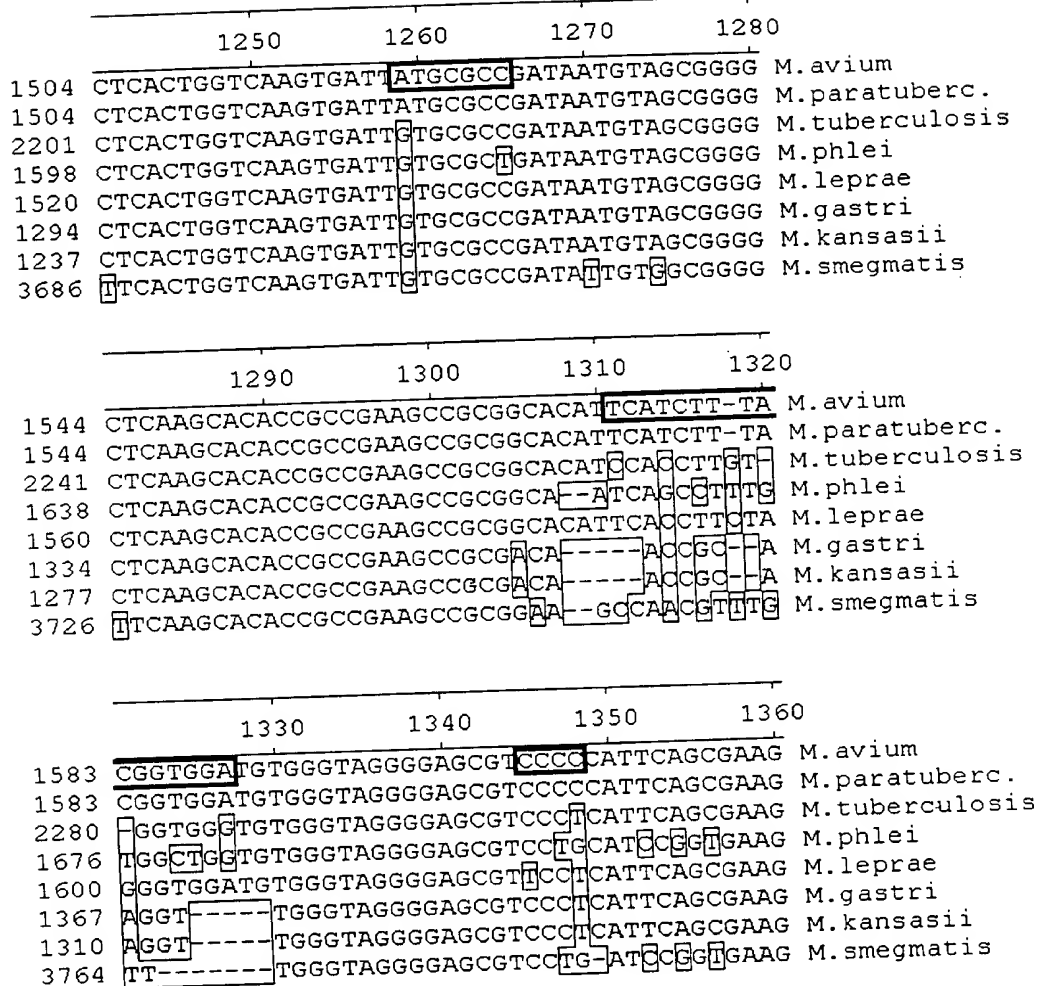


Figure 4F

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1370 1380 1390 1400

1623 CT-CCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT M.avium
 1623 CT-CCGGGTGA[□]CGGTGGTGGAGGGTGGGGGAGTGAGAAT M.paratuberc.
 2319 CCACCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT M.tuberculosis
 1716 CCGCCG[□]AGTGA[□]CGGTGGTGGAGGGT[□]GGGAGTGAGAAT M.phlei
 1640 CCTCCGGGT[□]ACCGGTGGTGGAGGGTGGGG[□]AGTGAGAAT M.leprae
 1402 CCGCCGGGTGACCGGTGGTGGAGG[□]TGGGGAGTGAGAAT M.gastri
 1345 CTGCCGGGTGACCGGTGGTGGAGG[□]TGGGGAGTGAGAAT M.kansasii
 3796 CCGCCG[□]AGTAT[□]CG[□]AGTGGTGGAGGGT[□]GGGAGTGAGAAT M.smegmatis

- - - -

1530 1540 1550 1560

1781 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT[□]ATGGG M.avium
 1781 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG M.paratuberc.
 2479 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT[□]TGGG M.tuberculosis
 1875 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATG[□]AG M.phlei
 1800 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT[□]TGG[□] M.leprae
 1562 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT[□]TGGG M.gastri
 1505 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT[□]TGGG M.kansasii
 3956 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATG[□]G M.smegmatis

1570 1580 1590 1600

1821 CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG M.avium
 1821 CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG M.paratuberc.
 2519 CG[□]CC[□]GTGA[□]GAATCA-GCGGTACTAACCACCCAAAACCG M.tuberculosis
 1915 CGTCCCTGATGAATCA[□]TCATT[□]T[□]GCTAACCACCCAAAACCG[□] M.phlei
 1840 CG[□]CC[□]GTGAATCA-GCGGTACT[□]ACCACCCAAAACCG M.leprae
 1602 CG[□]CC[□]GTGAATCA-GCGGTACTAACCACCCAAAACCG M.gastri
 1545 CG[□]CC[□]GTGAATCA-GCGGTACTAACCACCCAAAACCG M.kansasii
 3996 CGTCC[□]ATGAATCA-GCGGTACTAACC[□]CCAAAACCG[□] M.smegmatis

Figure 4G

23/31

	1610	1620	1630	1640	
1860	GAT-CGATCCAT-T	CCCCCTTCGGGGG	C-GTGGCGATT-C	GG	M. avium
1860	GAT-CGACCAT-T	CCCCCTTCGGGGG	C-GTGGCGATT-C	GG	M. paratuberc.
2558	GAT-CGATCA	TCCCCCTTCGGGGG	TGTGGAGTT	TGG	M. tuberculosis
1955	GAT-CGATC	ATCC	TTCGGGG	GTGACGGTTG	GG
1879	GAT-CGACCAT	TCCCCCTTCGGGGG	CTATGGAGGTT	CGG	M. leprae
1641	GAT-CGATCAC	TCCCCCTTCGGGGG	A-GTGGAGGTC	TGG	M. gastri
1584	GAT-CGATCAC	TCCCCCTTCGGGGG	C-GTGGAGGTC	TGG	M. kansasii
4035	ACCGTGACCG	CACT	TTCGGGG	TGTGGCGTTGGTGG	M. smegmatis

	1650	1660	1670	1680	
1896	GGCTGCGTGG	GACCTTCGC	TGGTAGTAGTCAAG	AATGGG	M. avium
1896	GGCTGCGTGGG	ACCTTCGCTGGTAGTAGTCAAG	CAATGGG		M. paratuberc.
2594	GGCTGCGTGGGA	ACTTCGCTGGTAGTAGTCAAG	CGATGGG		M. tuberculosis
1986	GGCTGCGTGGG	ACCG	GTGGTAGTAGTCAAG	CGATGGG	M. phlei
1917	GGCTGCGTGGGA	ACTTCG	TGGTAGTAGTCAAG	CGATGGG	M. leprae
1677	GGCTGCGTGGG	ACCTTCGCTGGTAGTAGTCAAG	CGATGGG		M. gastri
1620	GGCTGCGTGGG	ACCTTCGCTGGTAGTAGTCAAG	CGATGGG		M. kansasii
4071	GGCTGCA	TGGGACCTTCG	TGGTAGTAGTCAAG	CGATGGG	M. smegmatis

	1690	1700	1710	1720	
1936	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. avium
1936	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. paratuberc.
2634	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M. tuberculosis
2025	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M. phlei
1957	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M. leprae
1717	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. gastri
1660	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. kansasii
4111	-GTGACGCAGGAAGGTAGCCGTACC	GTGTCAGTGGTAATA-			M. smegmatis

	1730	1740	1750	1760	
1974	-CTGGGGCAAGCC	CGTAG--	AGAGCGATAGGCAAATCCGT		M. avium
1974	-CTGGGGCAAGCCCGTAG--	AGAGCGATAGGCAAATCCGT			M. paratuberc.
2672	-CTGGGGCAAGCC	GTAGGG	AGAGCGATAGGCAAATCCGT		M. tuberculosis
2063	-CTGGGGCAAGCC	GTAGGG	GAGTATAGGCAAATCCGT		M. phlei
1995	-CTGGAGCAAGCCCGTAGGG	AGAGCGATAGGCAAATCCGT			M. leprae
1755	-CTGGGGCAAGCC	GTAGGG	AGAGCGATAGGCAAATCCGT		M. gastri
1698	-CTGGGGCAAGCC	GTAGGG	AGAGCGATAGGCAAATCCGT		M. kansasii
4149	-CTGGCGTAAGCC	GTAGGG	AGTCAATAGG	CAAATCCGT	M. smegmatis

Figure 4H

24/31

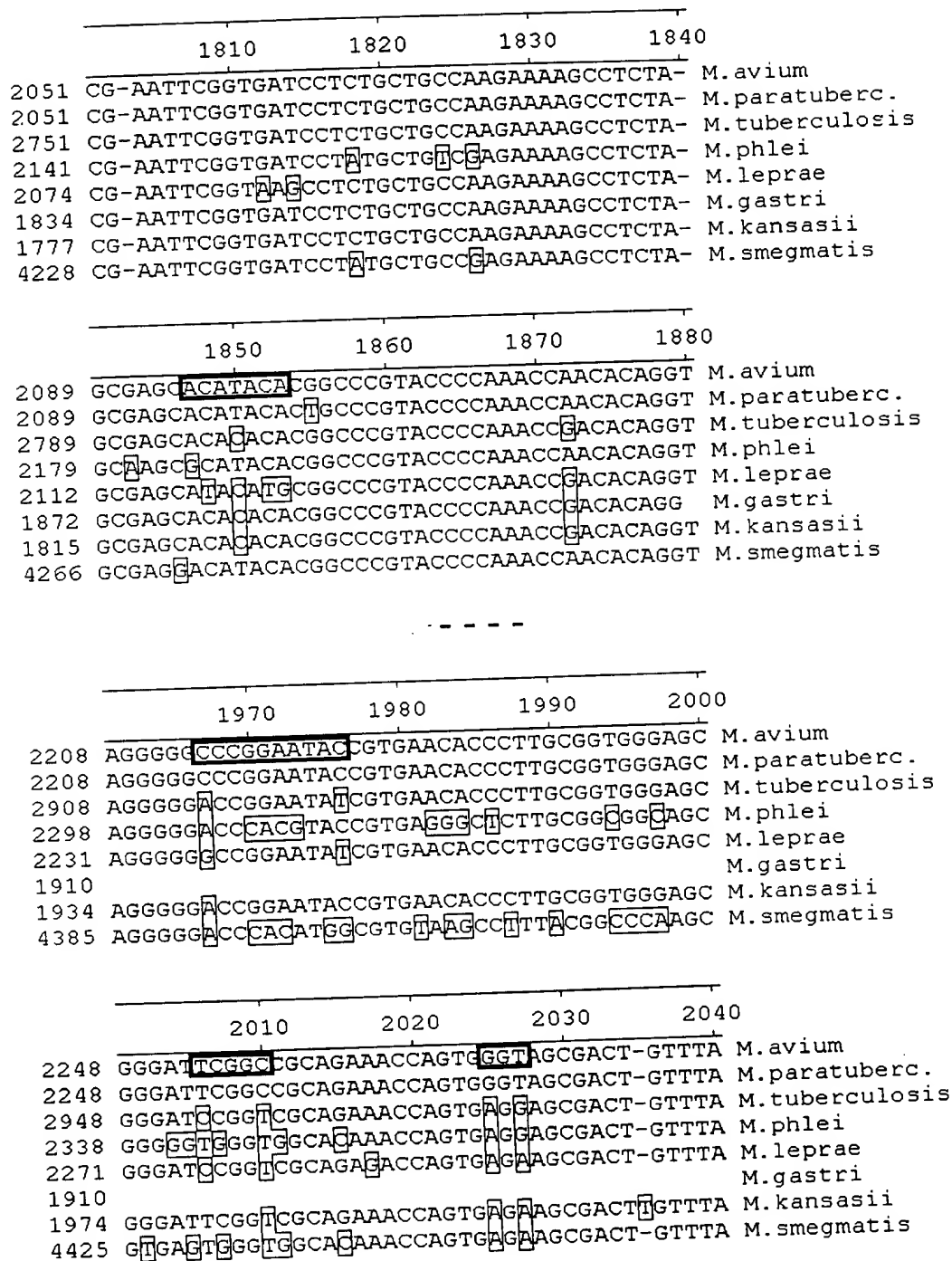


Figure 4

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	2130	2140	2150	2160	
2367	CCGTTAACCC	GT	--AAGGGTGAAGCGGAGAATTTAAGCCC		M.avium
2367	CCGTTAACCCGT	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.paratuberc.
3067	CCGTTAACCCG	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.tuberculosis
2457	CCGTTAACCC	TTTCGGGGGTGAAGCGGAGAATTTAAGCCC			M.phlei
2390	CTGTTAACCCGA	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.leprae
1910					M.gastri
2094	CCGTTAACCCG	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.kansasii
4544	CCGTTAACCC	CCTTGGGGGTGAAGCGGAGAATTTAAGCCC			M.smegmatis

	2250	2260	2270	2280	
2485	GTAACGACTTC	CCAA	CTGTCTCAACCATAGACTCGGCGAA		M.avium
2485	GTAACGACTTCCCAACTGTCTCAACCATAGACTCGGCGAA				M.paratuberc.
3185	GTAACGACTTCTCAACTGTCTCAACCATAGACTCGGCGAA				M.tuberculosis
2577	GTAACGACTTCTCAACTGTCTCAACCATAGACTCGGCGAA				M.phlei
2508	GTAACGACTTCTCAACTGTCTCAACCATAGACTCGGCGAA				M.leprae
1910					M.gastri
2212	GTAACGACTTCTCAACTGTCTCAACCATAGACTCGGCGAA				M.kansasii
4663	GTAACGACTTCTCAACTGTCTCAAC	ATAGACTCGGCGAA			M.smegmatis

	2370	2380	2390	2400	
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTTGAA			M.avium
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACTTTTGAA				M.paratuberc.
3305	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.tuberculosis
2697	GTCGATACGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.phlei
2628	GTTTCGGTTCGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.leprae
1910					M.gastri
2332	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.kansasii
4782	GTCGATACGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.smegmatis

Figure 4J

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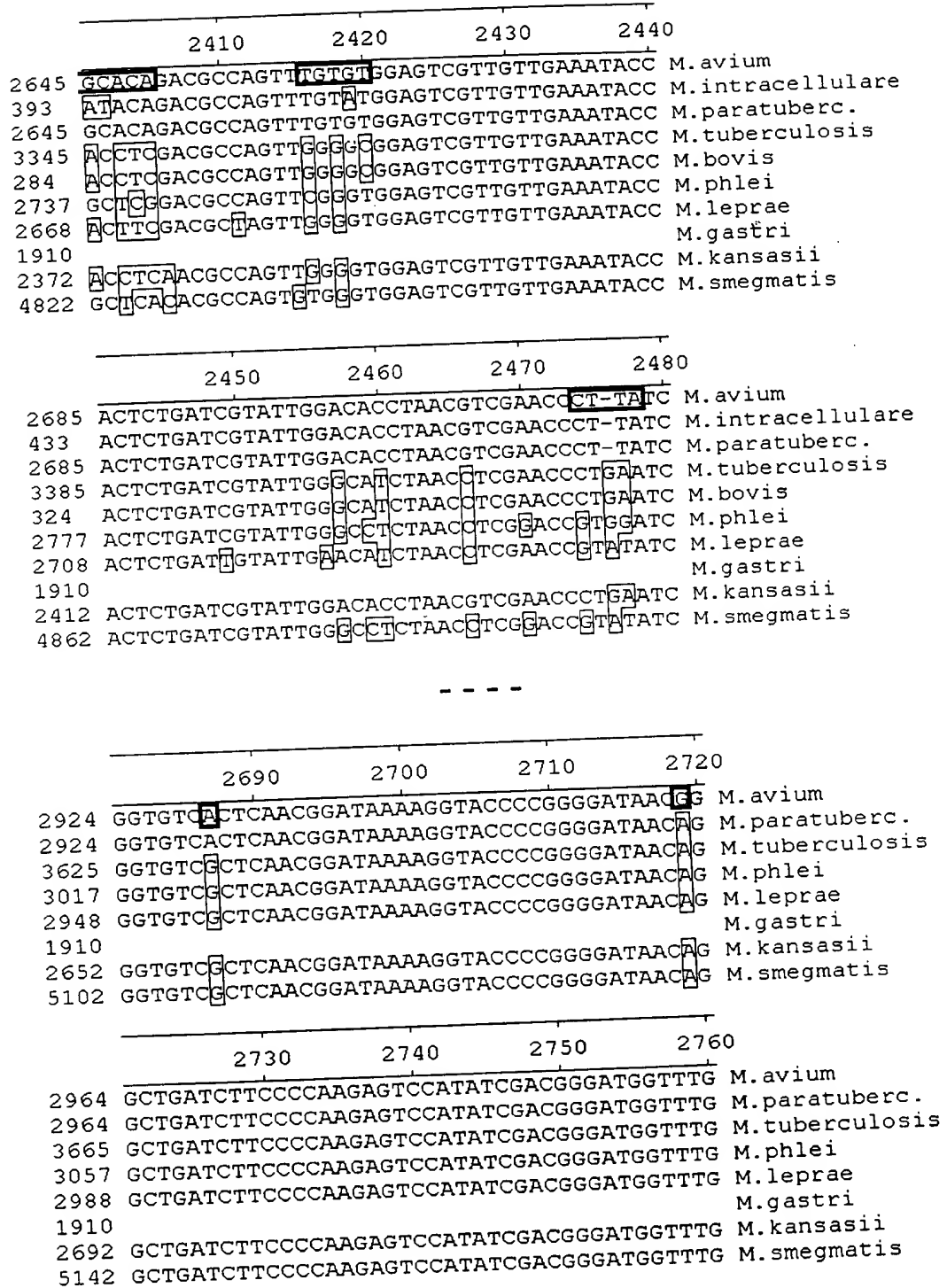


Figure 4K

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	2770	2780	2790	2800	
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. avium
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. paratuberc.
3705	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. tuberculosis
3097	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. phlei
3028	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. leprae
1910					M. gastri
2732	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. kansasii
5182	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. smegmatis
	2810	2820	2830	2840	
3044	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. avium
3044	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. paratuberc.
3745	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. tuberculosis
3137	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. phlei
3068	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. leprae
1910					M. gastri
2772	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. kansasii
5222	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. smegmatis

	3050	3060	3070	3080	
3283	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. avium
638	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. intracellulare
3283	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. paratuberc.
3984	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. tuberculosis
570	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. bovis
3376	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. phlei
3307	CAA				M. leprae
1910					M. gastri
3011	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. kansasii
5462	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. smegmatis
	3090	3100	3110	3120	
3322	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. avium
677	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. intracellulare
3322	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. paratuberc.
4023	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. tuberculosis
609	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. bovis
3415	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. phlei
3309					M. leprae
1910					M. gastri
3050	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. kansasii
5501	CCCGC-AGACCACGGGATTGATAGGCAGACCTGGAAGCT				M. smegmatis

Figure 4L

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		130	140	150	160	
107	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.avium
59	GAGTAACACGTGGGCAATCTGCCCTGCACTTC	-GGGATAA				M.intracellulare
107	GAGTAACACGTGGGCAATCTGCCCTGCACTTC	-GGGATAA				M.paratuberc.
70	GAGTAACACGTGGGCAATCTGCCCTGCACTTC	-GGGATAA				M.scrofulaceum
70	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.tuberculosis
209	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.bovis
120	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.leprae
69	GAGTAACACGTGGGCAATCTGCCCTGCACACC	-GGGATAA				M.kansasii
70	GAGTAACACGTGGGCAATCTGCCCTGCACACC	-GGGATAA				M.gastri
104	GAGTAACACGTGGG	CA	ATCTGCCCTGCACATC	-GGGATAA		M.gordonae
64	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.marinum

		450	460	470	480	
424	AAACCTCTTTCACCATCGACGAAGGTCCGGG	TTTT	CTCGG			M.avium
376	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTTTCTCGG					M.intracellulare
424	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTTTCTAGG					M.paratuberc.
387	AAACCTCTTTCACCATCGACGAAGGTCTCA---CTTCTGG					M.scrofulaceum
389	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTCTCTCGG					M.tuberculosis
528	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTCTCTCGG					M.bovis
439	AAACCTCTTTCACCATCGACGAAGGTCTGGGATTCTCTCGG					M.leprae
386	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTCTCTCGG					M.kansasii
387	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTCTCTCGG					M.gastri
420	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTTTCTCGG					M.gordonae
381	AAACCTCTTTCACCATCGACGAAGGTCTGGGTTTTCTCGG					M.marinum

		490	500	510	520	
429	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.tuberculosis
568	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.bovis
464	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.avium
416	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.intracellulare
464	ATTGACGGTAGGTGGAGAAGAAGCAC-----ACTACGTG					M.paratuberc.
424	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.scrofulaceum
479	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.leprae
426	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.kansasii
427	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.gastri
460	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.gordonae
421	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.marinum

Figure 5A

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	1130	1140	1150	1160	
1104	TCTCATGTTGCCAG	GGGTAATGC	CGGGGACTCGTGAGAG		M.avium
1056	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.intracellulare
1098	TCTCATGTTGCCAGCGGGTAATGC	GGGGACTCGTGAGAG			M.paratuberc.
1064	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.scrofulaceum
1069	TCTCATGTTGCCAGCA	CGTAATG	STGGGGACTCGTGAGAG		M.tuberculosis
1208	TCTCATGTTGCCAGCA	CGTAATG	STGGGGACTCGTGAGAG		M.bovis
1119	TCTCATGTTGCCAGCA	CGTAATG	STGGGGACTCGTGAGAG		M.leprae
1066	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.kansasii
1067	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gastri
1100	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gordonae
1061	TCTCATGTTGCCAGCA	CGTAATG	STGGGGACTCGTGAGAG		M.marinum

- - - -

	1290	1300	1310	1320	
1264	CGAATCCTTTTAAAGCCGGACTCAGTTCGGAT	TGGGGTCT			M.avium
1216	CGAATCCTTTTAAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.intracellulare
1258	CGAATCCTTTTAAAGCCGGACTCAGTTCGGATTGGGGTCT				M.paratuberc.
1224	CGAATCCTTTTAAAGCCGG	CTCAGTTCGGAT	TGGGGTCT		M.scrofulaceum
1229	CGAATCCTTTA-AAAGCCGG	ICTCAGTTCGGAT	TGGGGTCT		M.tuberculosis
1368	CGAATCCTTTA-AAAGCCGG	ICTCAGTTCGGAT	TGGGGTCT		M.bovis
1279	CGAATCCTTTTAAAGCCGG	ICTCAGTTCGGAT	TGGGGTCT		M.leprae
1226	CGAATCCTTTTAAAGCCGG	ICTCAGTTCGGAT	TGGGGTCT		M.kansasii
1227	CGAATCCTTTTAAAGCCGG	ICTCAGTTCGGAT	TGGGGTCT		M.gastri
1260	CGAATCCTTTTAAAGCCGG	ICTCAGTTCGGAT	TGGGGTCT		M.gordonae
1221	CGAATCCTTTA-AAAGCCGG	ICTCAGTTCGGAT	TGGGGTCT		M.marinum

	1330	1340	1350	1360	
1304	GCAACTCGACCCCA	TGAAGTCGGAGTCGCTAGTAATCGCA			M.avium
1256	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.intracellulare
1298	GCAACTAGACCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.paratuberc.
1264	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.scrofulaceum
1268	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.tuberculosis
1407	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.bovis
1319	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.leprae
1266	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.kansasii
1267	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.gastri
1300	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.gordonae
1260	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.marinum

Figure 5B

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2550 | TTACGGCGGCAGGACGAAAAGACCCCGGGACCTTCACTA 2589 |
2568 2569 |

Mavirus 23S:

Figure 6

441 | TGGAGAGAGAGCACCAGGCGCCAACTACGTGCCAGCAGCGGGGTAATACGTAG 491
452 | 473 474 477
843 | GTACCGCGCAAGGCTAAACTCAAGGAATTGACGGGGGC 883
863 866

M. tuberculosis 16S:

Figure 7